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AGENT-BASED SIMULATION OF DISEASE SPREAD ABOARD SHIP

by

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March 2005

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Extreme examples like the Spanish Flu pandemic of 1918 make clear the devastating impact that communicable diseases can have on military readiness. It is highly desirable to have models and tools that can be used to evaluate the course of a disease over time. These tools can help assess the effectiveness of strategies employed to contain the outbreak such as constraining movement, wearing protective gloves or masks, closing high traffic areas, etc. Armed with these tools, a medical practitioner can better assess the right course of action in a time critical situation.

The primary difficulty with creating models and simulations for this purpose is that disease spread depends upon the details of human behavior and environmental variables which are not accounted for in current mathematical models. The likelihood that a particular individual will catch a given disease depends upon such specifics as where he works, whom he interacts with, where he sleeps, what he eats, his habits of personal hygiene, etc. It is hypothesized that a software disease simulation can combine agents that mimic human behavior, a ship specific environment, and disease specific attributes to more accurately model the spread of disease aboard ship than a mathematical model.

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AGENT-BASED SIMULATION OF DISEASE SPREAD ABOARD SHIP

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ABSTRACT

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The primary difficulty with creating models and simulations for this purpose is that disease spread depends upon the details of human behavior and environmental variables which are not accounted for in current mathematical models. The likelihood that a particular individual will catch a given disease depends upon such specifics as where he works, whom he interacts with, where he sleeps, what he eats, his habits of personal hygiene, etc. It is hypothesized that a software disease simulation can combine agents that mimic human behavior, a ship specific environment, and disease specific attributes to more accurately model the spread of disease aboard ship than a mathematical model.

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TABLE OF CONTENTS

I. INTRODUCTION 1
A. RESEARCH OBJECTIVES 1
B. BACKGROUND 2
1. Basic Epidemiology 2
a. Brief History 2
b. Taxonomy 3
c. Means of Transmission 4
d. Stages of Infection 4
e. Vaccination 6
2. Mathematical Models 7
a. SIR Model 8
3. Biological Weapons 9
a. Current Threats 10
C. RELATED WORK 10
1. Deterministic Models 10
2. Stochastic Models 11
D. ORGANIZATION 12

II. ARCHITECTURE 15
A. SHIP MODEL DESIGN 15
1. Requirements 15
2. Compartments 15
3. Hatches 16
4. Ladders 16
B. PERSONNEL MODEL DESIGN 16
1. Requirements 16
2. Personnel Attributes 17
3. Behavior 17
4. Movement 17
C. DISEASE MODEL DESIGN 17
1. Modes of Transmission 17
2. Stages of Infection 17
3. Surface Survival 17
4. Precautions 18
a. Quarantine 18
b. Vaccination 18
c. Closing Spaces 18
d. Wearing Masks 18
e. Wearing Gloves 18

III. IMPLEMENTATION 19
A. DATABASE 19

1. Ship Model 19
2. Personnel Model 20
B. TIMESTEP 20
C. INPUTS 22
1. Virus Attributes 22
2. Precautions 24
3. Simulator 24
D. GUI 25
E. CHARTS 26
IV. TESTING AND ANALYSIS 29
A. DISEASE SCENARIOS 29
1. Smallpox 29
2. SARS 34
3. Norovirus 38
V. CONCLUSION 43
A. SUMMARY 43
B. FUTURE WORK 43
LIST OF REFERENCES 47
INITIAL DISTRIBUTION LIST 49

LIST OF FIGURES

Figure 1. The population size of an infectious agent replicating inside a host and classification of stages of infection (Nelson et al., 2001).....6
Figure 2. SIR model for a closed population (Nelson et al., 2001).....9
Figure 3. SIR system of differential equations (Nelson et al., 2001).....9
Figure 4. Graphical user interface.....26
Figure 5. Pie chart displaying infection causes.....27
Figure 6. Multi-series XY chart showing how many personnel are in each stage of the disease over time.....27
Figure 7. Smallpox parameters.....31
Figure 8. Comparison between restricting the sick (left) and not restricting the sick (right) during an outbreak of smallpox.....31
Figure 9. Comparison between the small pox base graph (left) the graph representing the effects of wearing gloves (right).....32
Figure 10.Comparison between the small pox base graph (left) and the graph representing the effects of vaccinating half the crew (right).....33
Figure 11.Comparison between the small pox base graph (left)and the graph representing a contact probability of one percent(right).....34
Figure 12.SARS parameters.....35
Figure 13.SARS basic graph.....36
Figure 14.Comparison between the SARS base graph (left) and the graph representing the combined effects of restricting the sick, wearing gloves, and wearing a mask (right).....37
Figure 15.Comparison between the SARS base graph (left) and the graph representing the effect of lowering removal time to ten days (right).....38
Figure 16.Comparison between the SARS base graph (left) and the effect of raising the removal time to twenty days (right).....38
Figure 17.Norovirus parameters.....40
Figure 18.Norovirus base graph.....41
Figure 19.Comparison between the norovirus base graph (left) and the combined effects of restricting the sick and wearing gloves (right).....41

Figure 20. Comparison between the norovirus base graph (left) and the graph representing the effects of a waterborne transmission probability of one percent (right) 42

LIST OF TABLES

Table 1. Effects of precautionary measures on the smallpox virus.....32
Table 2. Effects of precautionary measures on the SARS virus..37
Table 3. Effects of precautionary measures on the norovirus...42

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I. INTRODUCTION

> It is generally not possible to conduct repeated experiments involving outbreaks of an infectious disease (Becker, 1989, pg 2).

A. RESEARCH OBJECTIVES

The intended purpose of this thesis is to begin the long and daunting process of accurately simulating disease spread aboard Navy ships. The absence of complete shipboard disease spread data along with the complexities of shipboard personnel behaviors make the process problematic. The purely mathematic deterministic forms of simulation fail to allow for the many variables that human interaction aboard ship entails. The stochastic computer programs can deal with multiple forms of transmission, spatial and closed environments, heterogeneous group behaviors, and various precautionary measures.

The short term goal is to provide a health care provider with a useful decision support tool with a user friendly interface. This tool will provide an approximation of potential disease spread events. The approximation can help the provider to make a more informed decision which could save lives and salvage mission readiness in the event that the ship becomes infected with a serious disease.

This thesis is specific to ship board disease spread and should not be applied to open environments where humans are not contained in close quarters. Most forms of disease transmission are simulated, but not all. There are diseases spread via parasites and fungi to which this work does not apply despite their relevance to Navy Ships

(Mueller & Garland, 1989). Diseases spread via arthropods or other agents (vector-borne), by animals (zoonoses), through soil, blood, or sexually transmitted diseases are not modeled here. The main modes of transmission that are modeled are airborne, contact with an infected surface, or consuming contaminated food or water. These forms of transmission cover diseases such as the flu, small pox, norovirus, etc.

The proper use of the Java program describe in this work requires a detailed database containing the ship compartmental information specific to each ship, along with a detailed personnel database which includes the routine of each individual. The routine can be generalized by knowing the rate of the individual and standardizing normal routine according to rate. The ship compartment information should be entered by a subject matter expert that has access to ship blueprints. The personnel database should be managed by the Personnel or Administration Department of the ship. The sole responsibility of the medical practitioner should be to input the virus attributes, precautionary measures, run the simulation, and interpret the results. The details of these inputs will be covered in chapter III.

B. BACKGROUND

1. Basic Epidemiology

a. Brief History

Disease has been around since the beginning of time. It is one of the primary checks on population, the others being war, famine, and natural disasters.

> Were there no other depopulating causes, every country would, without doubt, be subject to periodical pestilences or famine. (Malthus, 1798, pg 48)

The study of how and why diseases spread is as timeless as war. It is natural to investigate why people get sick; the most obvious reason is to prevent further sickness. The earliest recorded diseases are smallpox, leprosy, tuberculosis, meningococcal infections, and diphtheria (Nelson, Williams, & Graham, 2001). Smallpox is speculated to have existed as early as 430 BC (Cartwright, 1972). The Bubonic Plague, coined the "black death", is another example of how devastating disease can be. Some say it is the greatest European catastrophe in history (Cartwright, 1972). The most pertinent past disease to this thesis is the Spanish Flu, which killed twenty to forty million people worldwide (Billings, 1997). It occurred in 1918 towards the end of World War II and made a huge impact on military readiness. It is common for diseases to have more effect on children or the elderly. The Spanish Flu mostly affected people from the ages of twenty to forty. In today's military, the mean age of officers is thirty-four and enlisted twenty-eight (Personnel & Readiness, 1997) making most personnel within the susceptibility range of the Spanish Flu.

b. Taxonomy

The microorganisms responsible for disease are broken down via genetic characteristics. The main groups, viruses, bacteria, fungi, and parasites, are listed below.

A virus is the smallest of the infectious agents. They contain a single form or type of nucleic acid, either DNA or RNA. They are obligate intracellular parasites, and their replication is host-cell-dependent directed by their DNA. There are viruses specific for almost every organism (Nelson et al., 2001). Examples of viruses are yellow

fever, influenza, measles, HIV, coronaviruses and small pox.

Bacteria are single celled organisms that can survive incredible temperature extremes. Some can survive temperatures above the boiling point of water and temperatures below freezing. Bacteria examples include: anthrax, diphtheria, tuberculosis, cholera, and pneumonia are commonly known bacterial diseases.

Fungi which are responsible for many of the skin and hair diseases, and parasites are not covered in this thesis. Their reservoir and transmission are not compatible with this model.

c. Means of Transmission

There are various ways to transmit a disease to a human, they are: airborne, vector-borne, perinatal, food or water-borne, or through contact. In this thesis, transmission that occurs from a mother to her child during pregnancy or at the time of delivery (perinatal), and vector-borne transmission via an arthropod (insect, mollusk, etc), are not covered. The three transmission methods covered are airborne, food or water-borne, and through physical contact. Airborne diseases are spread by the inhalation of contaminated air particles. Food and waterborne transmission occurs through ingestion of contaminated food or water. Contact transmission takes place with direct or indirect contact with an infected surface, blood or body fluid.

d. Stages of Infection

The interaction between an infected human and a disease have various stages. The time and duration that these stages occur are unique to the individual and disease

combination, see Figure 1. Each person has different tolerances based on prior exposure, age, and health. Despite this variability, each virus strain seems to affect people in a predictable enough way to estimate when these stages begin and end with reasonable variation.

A healthy non-infected person that has never come into contact with the specific disease, or a similar form of it, is susceptible. Once infected with the disease, the individual may or may not progress into the infected stage. This depends on the amount of the disease agent and whether or not the live disease can reproduce faster than it is destroyed by the person's immune system. The latent and incubation periods occur immediately after the initial infection. When the latent period ends, the individual becomes contagious to others. When the incubation period ends, the individual begins showing symptoms. The latent and incubation periods do not always coincide. In other words, a person can be contagious well before showing symptoms. In some cases, the person could be asymptomatic, or without symptoms. An example of an asymptomatic disease is the AIDS virus; an infected person usually does not show symptoms for several years, before exhibiting the symptoms of an opportunistic disease. Once a person becomes infective or contagious, they either recover or die from the disease. Symptoms may not coincide with this recovery. For example, a person may still be contagious even after symptoms cease. The infected person either dies from the disease or recovers.

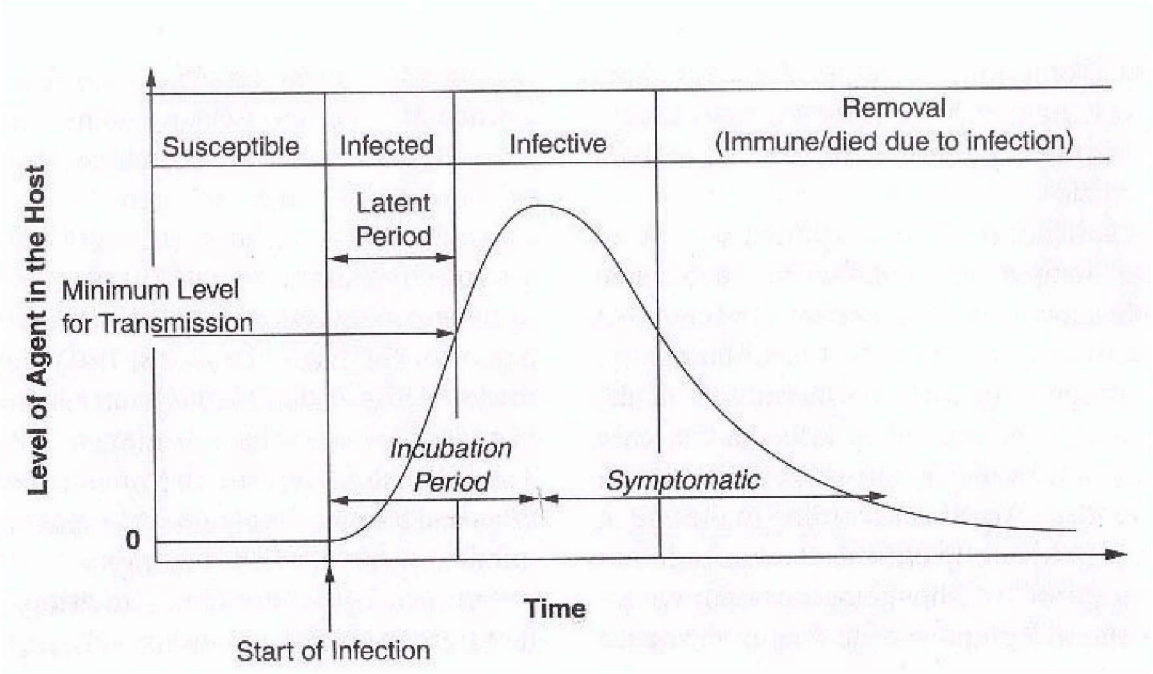

Figure 1. The population size of an infectious agent replicating inside a host and classification of stages of infection (Nelson et al., 2001).

e. Vaccination

When an infected host survives an infectious disease, a lifelong immunity is usually acquired. Even if the host survives, the price of this form of immunity could be permanent damage to the host's body. Rather than risking the life of an individual, vaccination is a solution that either prevents the effects of the disease, or lessens them through exposure to a weaker form of the disease.

> The first scientific attempt at vaccination occurred in 1796, when Edward Jenner proved that persons inoculated with cowpox were resistant to challenge with Variola virus, the etiologic agent responsible for smallpox. (Nelson et al., 2001, pg 255)

Vaccination has led to the eradication of once devastating diseases such as small pox and measles (Cartwright, 1972).

The efficacy of an active immunity vaccination depends on type, which can be a live attenuated organism, or a dead form. The live vaccine often provides lifelong immunity because the host does not differentiate between the vaccine and a natural exposure. This may lead to adverse affects in hosts with poor immune systems. An inactive vaccine provides short term relief and usually requires several doses since the disease does not reproduce.

An alternative to active immunity is passive immunity. It is performed through injection of human or animal antibodies, in the form of immune globulin, to fight the specific disease. This form of immunity is short term because it does not force the host to create its own antibodies. This type of immunity can be useful if the host has a high chance of coming into contact with the disease without enough time for a vaccination to assure adequate immune response.

2. Mathematical Models

> A mathematical model is an explicit mathematical description of the simplified dynamics of a system (Nelson et al., 2001, pg 150)

Modeling a disease is very difficult since acquiring complete and detailed data is rare (Becker, 1989). The lack of detailed data makes it hard to provide valid assumptions for an accurate mathematical model. The lack of validated assumptions leads epidemiologists to use simplified mathematical models. A population may contain

several distinct groups, yet these groups are aggregated for simplicity. By aggregating groups of people that may have different behaviors and interactions, a significant level of detail is lost. On the other hand, creating a mathematical model that contains variables for each group has its own problems.

If a significantly complex mathematical model is created to represent the spread of disease, it would contain so many variables that few could understand it. In fact, even if a complex mathematical model provides an improved approximation of disease spread, it may not be interpretable.

> Although the model suppresses a great deal of detail, it is complicated enough to make understanding difficult. When you discover some new aspect of its behavior, it can be difficult to track down the mechanism responsible. Thus, adding more structure in the cause of realism would not necessarily teach us much. We might well reach a point where we could not understand the model any better than we understand the real world. (Nelson et al., 2001, pg 167)

The disease simulator introduced in this thesis contains many variables and is similar to a complex mathematical model. The difference is the ease of use, interpretability and the capacity to assess precautionary measures. For a mathematical model, these precautionary measures require additional variables and entail interactions that add significant complexity.

a. SIR Model

The (Susceptible-Infected-Recovered) SIR model (Kermack & McKendrick, 1927) is a system of three differential equations that determine the number of people in one of three categories: susceptible, infective, or

removed, see Figure 2 & 3. The contact parameter β incorporates the area of movement and probability of contact between a susceptible and an infective. The γ is the rate at which an infective recovers (Nelson et al., 2001). N represents the total population, made up of either susceptibles, infectives, or removals.

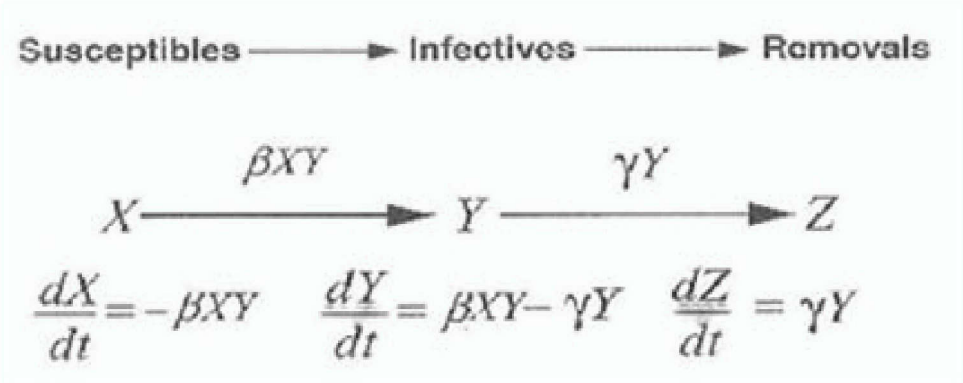

Figure 2. SIR model for a closed population (Nelson et al., 2001).

$$\frac{dX}{dt} = -\beta XY$$
$$\frac{dY}{dt} = \beta XY - \gamma Y$$
$$\frac{dZ}{dt} = \gamma Y$$
$$X + Y + Z = N$$

Figure 3. SIR system of differential equations (Nelson et al., 2001).

3. Biological Weapons

A biological warfare weapon uses living disease causing agents to infect its target (Croddy, 2002). The intended effect is death or injury causing loss of military readiness and troop strength. Due to the heinous nature

of biological weapons it is uncommon for a country using them to claim responsibility.

> The first allegations were made against German attempts to employ biological agents during World War I (Cookson & Nottingham, 1969, pg 54).

Apparently there was evidence that in 1915 they inoculated horses and cattle leaving U.S. ports for shipment to the Allies with disease-producing bacteria (Cookson & Nottingham, 1969). The Japanese and Russians were also known for their chemical and biological warfare production.

a. Current Threats

Currently, biological agent production is feared to be widespread. It is the delivery capability that is unknown. For chemical or biological weapons to be effective, they must be delivered properly. Although for a ship board problem to occur, only one crew member needs to be infected to produce negative effects.

Pertinent ship threats include food and waterborne diseases (Adak, Meakins, Yip, Lopman, & O'Brien, 1996-2000) and the fear of a small pox resurgence.

C. RELATED WORK

There are two distinct approaches to modeling disease spread. One approach is to use a deterministic model which is inherently mathematical with no probability involved. The other approach is stochastic and is based upon probabilities.

1. Deterministic Models

These models do not contain any form of probability. The model will have the same output given the same input consistently from one run to the next. They are mathematical, in the form of equations.

In a simulation of the severe acute respiratory syndrome (SARS), Wang & Ruan(2003) fit existing data from an outbreak in Beijing to create a deterministic model. They use six classes or states, susceptible, exposed, quarantined, suspect infective, probable infective, and removed, to identify the status of each person. Despite the lack of data, the model seems to fit the existing data well. Variances are accounted for by variables such as precautions that are taken, activities and behaviors. These types of variables could be included in a more complex model, although it would likely be stochastic. It should also be noted that preexisting data is necessary to repeat this technique for a different disease. It is therefore a reactionary process which may not prove useful in unique situations or in situations involving new diseases where data is non-existent.

2. Stochastic Models

Most disease spread models have some form of probability involved, making them stochastic. The three works that were most pertinent to this thesis each have different characteristics. I will go over each of them.

Muller, Grebaut, & Gouteux, (2003), simulated human behavior using agents in an open environment that involved vector-borne disease spread. In this case, tsetse flies were the vector with animals and human beings the reservoir. The time step for the simulation was twelve hours. The agents move according to their age and position in the village. The model also uses agents to supervise other agents. The human behavior aspect is similar to this thesis.

One work used the Java programming language (Aschwanden, 2004) and state representation similar to the SIR model. These aspects are similar to this thesis. The similarity to the SIR model is purely for naming of states. The differential equations of the actual model are not utilized. People are grouped according to social function and movement is managed by this function. Some parameters are entered by the user, but others are preset. The input method for these preset parameters such as a person's social function is not mentioned. Various precautionary measures are mentioned, but not implemented. The resulting runs are not consistent. This is highly likely when using a stochastic model due to probability and the multiple interactions. One remedy which is implemented in this thesis is running the simulator multiple times and averaging values to provide a more robust result.

An implementation of military disease spread in a closed environment was done by Paterson, 2002. The disease transmission was person to person. The nature of the spread, airborne or contact, was not delineated. The susceptible, exposed, infected, and recovered (SEIR) model was used which is a variation of the SIR model. Microsoft Excel was utilized to calculate the results of discrete SEIR equations. Interactions between different groups were also input via spreadsheet. Time is advanced manually by the user in twenty four hour increments. Excel provides ease of use, but is limited as a programming method.

D. ORGANIZATION

There are five chapters in this thesis including the introduction. Chapter II describes the architecture of the disease simulation. Chapter III describes the specific

design of the disease simulation program. Chapter IV summarizes results of a series of runs varying virus parameters. It also assesses how precautions affect each scenario. Four scenarios are analyzed, small pox, norovirus, SARS, and the flu. Chapter V contains the conclusions and provides recommendations for future work.

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II. ARCHITECTURE

The disease spread simulation described in this thesis has an architecture comprised of three models, the ship model, personnel model, and disease model. Each of these is described below.

A. SHIP MODEL DESIGN

1. Requirements

In order to create a ship model for real world use, the model must represent the specific type of ship. Each class of ship has different characteristics; An aircraft carrier is completely different from a frigate. The aircraft carrier has a landing deck, hangar, and control tower while a frigate or smaller ship is much simpler. Since no specific type of Navy ship was identified, a generic model is employed that is adaptable to nearly any ship type. The only condition is that it follows the basic rules of ship compartment nomenclature. When data is entered in the proper form, a spatially sound ship model is created.

2. Compartments

Ship compartments are basically the distinct physical locations aboard ship. Each compartment is identified using a specialized nomenclature. This naming system is standard aboard Navy ships. It is essential to know the system to be able to navigate from place to place.

A compartment's physical location is represented by three numbers in the following format: ##-##-##. The first number indicates which deck, or level, the compartment is located on. The second indicates the frame number of the forward bulkhead, or wall, of the compartment. Frame

numbers increase as you move aft, or to the rear, of the ship. The third number indicates the location of the compartment relative to the ships centerline. Even numbers are used for port, or left side compartments. Odd numbers are used for starboard, or right side (Nomenclature, 1942).

3. Hatches

Hatches use the same naming system. Since hatches do not occupy a significant amount of space and are always associated with entering or leaving a compartment, they are treated as part of the pertinent compartment.

4. Ladders

Ladders also use the same naming system. They are the primary, if not only, means of changing decks.

B. PERSONNEL MODEL DESIGN

1. Requirements

In order to properly model personnel behavior aboard Navy ships, knowledge about specific rate, or job, interactions must be identified along with routines specific to each ship. Unlike most other environments, people must interact onboard a ship. It is a closed environment with a limited number of compartments, making it nearly impossible to refrain from contact with another person. Each person may have a different routine and interact with different people on a daily basis. The large number of variables necessary to model and simulate a complex behavior as a differential equation (solving either analytically or with generic ODE software) is too many to be practical. Aggregating behavior only loses important data. In order to feasibly create an application and to preserve valuable data, it must have a defined yet broad scope. This can be done by generalizing routine and interactions specific to rate and rank.

2. Personnel Attributes

Each person has a predefined routine based on their rate and rank. It is important to know where they are going next and where they are now. If infected, their current stage of the disease should be known.

3. Behavior

In order to model behavior in a structured yet unpredictable way, each person follows a combination of their predefined routine and random deviations from this routine. For example, randomized head, or lavatory break should be used.

4. Movement

Moving from place to place should not be done by teleportation. Without having to pass through other compartments, open hatches, and climb ladders, there is no spatial characteristic to the model. Therefore, the model must take into account what obstacles are encountered when going from point A to point B.

C. DISEASE MODEL DESIGN

1. Modes of Transmission

The most prevalent modes of transmission, airborne, waterborne, and contact, should be addressed. These modes of disease transmission cover most pertinent diseases.

2. Stages of Infection

The pertinent stages of infection are the latent, incubation, contagious, symptomatic, and removed periods. The removal period encompasses both the immune and dead personnel.

3. Surface Survival

How long a disease survives when transmitted to an object is necessary to assess contact transmission.

4. Precautions

a. Quarantine

It is possible to quarantine an individual, but this solution is not always feasible. It may be better to model only realistic actions such as restricting the sick to their berthing, or sleeping quarters.

b. Vaccination

Inoculating individuals with a weakened form of a disease will help them to resist future infection. This effectively lowers the number of susceptible personnel on board the ship.

c. Closing Spaces

If a space becomes infected with a deadly disease and needs to be sanitized or is prone to disease spread, there should be a capability to close it.

d. Wearing Masks

Wearing a protective mask that covers the nose and mouth should filter airborne illnesses.

e. Wearing Gloves

Wearing protective gloves may lessen contact transmission.

III. IMPLEMENTATION

The implementation of the disease spread simulation described in this thesis was conducted with the end user in mind. The ship's medical practitioner should only have to deal with the elements of the simulation within his or her area of expertise. The disease's stages and virulence fit into this expertise. The details concerning compartment location and size should be left to a subject matter expert that is familiar with the ship layout and design. A database of people on board and their current routine should be maintained by the Personnel or Administration department. The methods employed and the instructions for using the simulation are described below.

A. DATABASE

The ship and personnel information are complex and changeable. A database is the commonly used form for information management. Databases can easily be managed via a database program such as Microsoft Access. Java Database Connectivity (JDBC) is used to connect to a Microsoft Access database that is registered as an Open Database Connectivity (ODBC) source. Access databases are used for ship and personnel data.

1. Ship Model

The ship model need only be entered once, unless compartments are modified. Pertinent information that is entered is location (in the proper form mentioned in chapter II), size, whether or not the room contains food or water, if the room or hatch is infected, and the location of the nearest head. The location information is used to determine where the compartment is for navigation purposes.

The size of the compartment is needed to determine likelihood that an airborne disease is transmitted. A smaller size compartment has a higher likelihood of passing on an airborne disease. The infection status of the room and hatch can be used to set a room or hatch infected prior to starting the simulation. The location of the nearest head is used to determine where the person goes when a random head break is necessary.

2. Personnel Model

Personnel information should be updated whenever crew members join or leave the ship. This is necessary in order to keep the simulation as situation specific as possible. This information contains name, rank, rate, infection status, immunity to a specific disease, shift (day or night), and routine. The routine is a fixed sequence of locations the individual goes to based on the time of day. The routine contains a workspace, mess (dining) hall, berthing, and formation. Routine is used for movement and affects interaction between crew members. Whether or not two crew members interact depends on if their routines coincide. Interaction is predetermined, except for random head breaks. Rank and rate can be used to make assumption regarding routine information if the individual cannot be asked directly. The infection status can be used to set a person infected if they are actually sick at the time the simulator is run. The immunity information can only be used for one disease. It determines who starts out as removed at the start of the simulation. The shift determines the time the crew member's working day begins.

B. TIMESTEP

The disease spread simulation updates the disease progression once per time unit. Each time unit represents

thirty minutes. For each time unit, there is a cycle of events. These events are as follows:

- Are crew members infected in their current location? – Each compartment has a status of infected or not infected. If a compartment is infected and susceptible (non-infected) crew members are located there, they can be infected based on the relevant transmission probability.
- Where do they move next? – Based on the crew member's shift, routine, and the time of day, their next location is determined. There is also a chance of the crew member's visiting the head or gym randomly. These visits can occur during any time of the day. The probability of these visits can be set within the program code. Gym visit probability is based on the likelihood that the crew member will find the time to work out throughout the week.
- Does a contagious crew member infect their current location? – A compartment can become infected either by marking it infected in the ship database or by a contagious crew member. If the disease is spread by contact with contaminated objects, food, or water, the compartment is infected for the surface survival time set by the user. This time is reset if re-infected. If the disease is transmitted by the air, it is infected if one or more contagious crew member is currently in the compartment.
- Is there infection caused on the way to the next location? – Depending on the crew member's current and next locations, they will climb specific ladders

and open certain hatches. If a crew member is contagious, they may infect hatches and ladders that are encountered. If a crew member is susceptible, they may become infected if an encountered hatch or ladder is infected. The contact transmission probability determines whether or not infection occurs.

- Do infected crew members change state (disease stage)? – All crew members, except those set infected in the personnel database or vaccinated at the simulation start, are initially susceptible. Each crew member's status is updated to: infected, latent, incubating, contagious, symptomatic, immune, or dead based on the disease periods specified by the medical practitioner. This is done by keeping track of the time that has passed since initial infection.

C. INPUTS

In addition to the databases, the necessary inputs to run the simulation are listed below. These inputs should be entered by a medical professional.

1. Virus Attributes

In order to describe a disease properly, the following inputs are needed:

- Airborne probability – The percent chance that the disease is transmitted in the airborne form when in close proximity to an infected crew member in a thirty minute period.

- Contact probability – The percent chance that the disease is transmitted by coming into contact with an infected surface in a thirty minute period. This probability includes the chance that contact is made.
- Waterborne probability – The percent chance that the disease is transmitted by food or water in a thirty minute period. This chance is amplified when in the mess hall or head.
- Surface survival time – The amount of time in days and hours that an infected surface remains infected. This time can be due to natural causes like evaporation, or to clean up.
- Incubation period – The mean amount of time, after infection, in days and hours required before symptoms occur.
- Latent period - The mean amount of time, after infection, in days and hours required before becoming contagious.
- Removal period - The mean amount of time, after infection, in days and hours required to become immune or dead.
- Fatality percent – The percent chance that an infected person will die from the disease.
- Vaccination percent – The percentage of the crew that is effectively vaccinated.

2. Precautions

While running the simulation, the medical practitioner can use the following precautions to see how the course of the disease is affected.

- Restrict sick – This precaution prevents movement of symptomatic personnel from their berthing. The only exception is to go to the head.
- Wear gloves – This precaution mandates the use of protective gloves when touching any potentially infected surfaces.
- Wear Mask – This precaution mandates the use of protective masks to prevent airborne transmission.
- Close the gym – This precaution terminates the use of a public space, available to all crew members, to prevent spread.

3. Simulator

The simulator itself has options. The options available to the medical practitioner are as follows.

- Initial start time - The hour that the simulation begins. This can be a number between zero and twenty three. For example, twenty three is equivalent to eleven PM.
- Number of runs – The number of times the simulation will run a complete scenario. The output will be averaged. The more runs, the more robust the outcome due to the stochastic nature of the simulation.

- Number of periods – The number of periods, given in days and hours, the simulation will run.

D. GUI

The graphical user interface (GUI) created for the disease spread simulation was focused around the medical practitioner's inputs, see Figure 4. Due to the need for valid input in order to properly run the simulation, each input received by the interface is checked for errors by the GUI. The following are the restrictions set on parameters:

- Airborne, contact, and waterborne probabilities need to have their respective checkbox selected. The values must be between 0.0 and 1.0.
- Surface survival, incubation, and latent times do not have a limited days field, but the hours field only accepts twenty three or less.
- The removal time must be greater than both the latent and incubation times. It does not have a limited days field, but the hours field only accepts twenty three or less.
- The fatality and vaccination percentages must be between 0.0 and 1.0.
- The precautions are simple check boxes.
- Initial start time is between zero and twenty three.
- The number of runs must be an integer value. It is not necessary to exceed one hundred.

- The number of periods is unlimited, but should be greater than the removal period to view the full course of the disease.

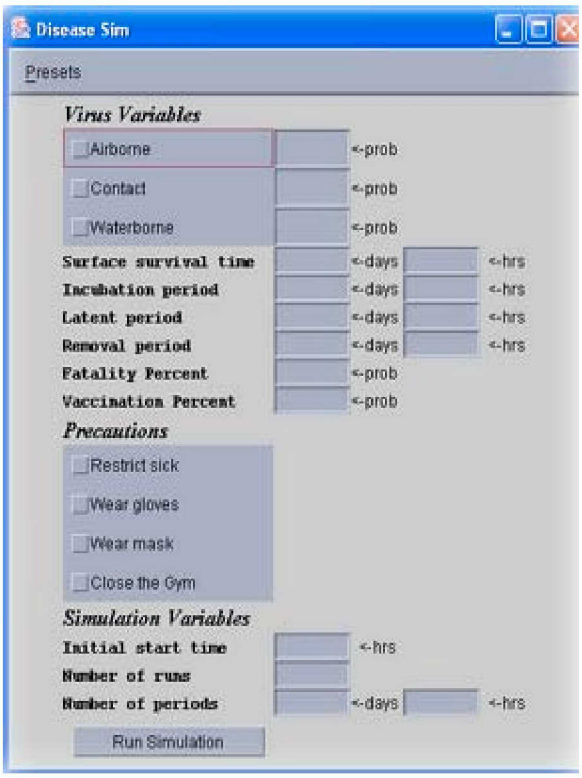

Figure 4. Graphical user interface.

The medical practitioner can also use the presets in the drop down box to automatically input the standard parameters for smallpox, SARS, and norovirus. Presets are also used as convenient starting points to configure the GUI for related diseases.

E. CHARTS

There are two charts used to display information about the course of the disease, a pie chart and a multi-series XY chart are displayed in Figures 5 & 6 respectively.

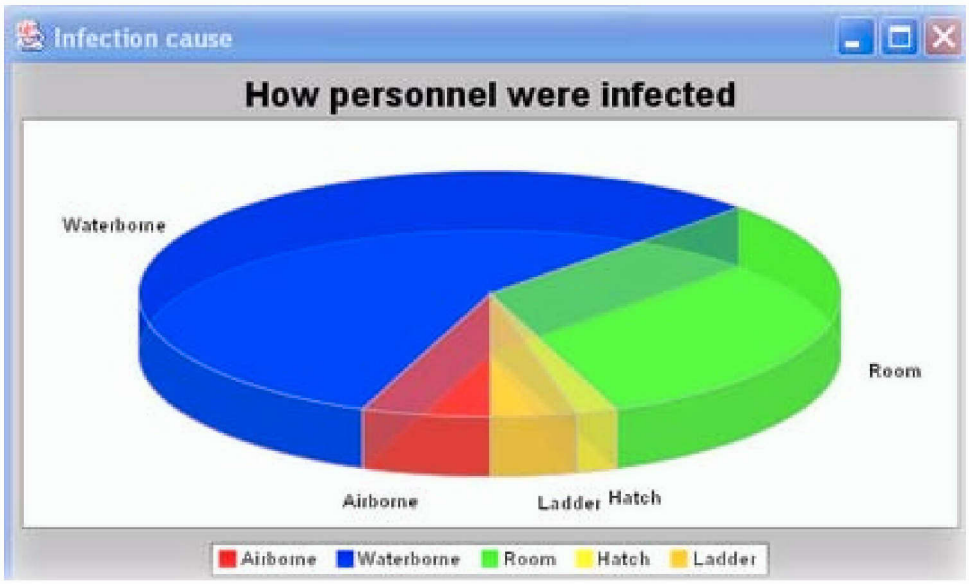

Figure 5. Pie chart displaying infection causes.

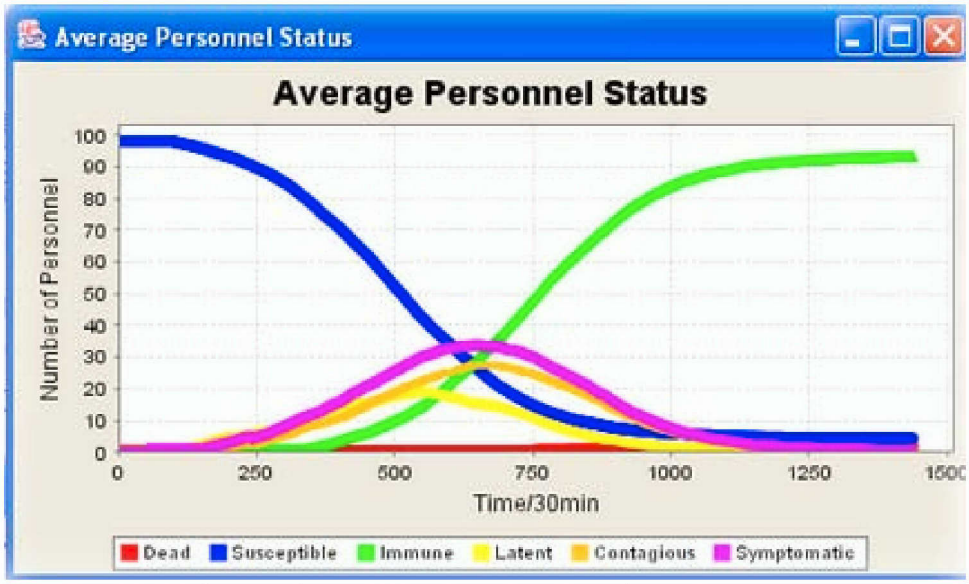

Figure 6. Multi-series XY chart showing how many personnel are in each stage of the disease over time.

The pie chart is used to show the percentage of people infected by different transmission methods out of the total infected. Contact transmission is broken up by location of infection: room, hatch, or ladder.

The multi-series chart displays the number of personnel in each stage of disease over time. Each stage is represented as separate series.

IV. TESTING AND ANALYSIS

A. DISEASE SCENARIOS

The ship board disease simulation was run under varied settings corresponding to three distinctly different diseases to identify trends and nuances in disease characteristics such as the number and rate of infection. Each setting was run one hundred times and the average output was used. Single runs yielded nearly identical results to the averaged output. The diseases addressed are smallpox, severe acute respiratory syndrome (SARS), and the norovirus. Each of these diseases will be described further in their respective sections. The settings that are changed include: precautionary measures taken, percentage vaccinated, and virulence of the disease transmission methods. The output is compared with a base output unique to the disease and differences are noted. Changes of interest are: maximum number of contagious at one time, total infected, rate of infection, duration of disease, number immune, and number dead.

1. Smallpox

> Smallpox is a serious, contagious, and sometimes fatal infectious disease. There no specific treatment … and the only prevention is vaccination (Smallpox, 2004).

Ordinary variola major is the most common form of small pox. This form will be used for the simulation. There is an overall fatality rate of approximately thirty percent. The virus is primarily transmitted through contact with contaminated objects such as clothing or bedding. It is rarely spread by airborne means. A person

infected takes seven to seventeen days for symptoms to begin. The host becomes contagious shortly thereafter (two to four days). The virus symptoms begin with an incapacitating fever (101-104 degrees Fahrenheit), followed by rash, bumps, pustules, and scabs. The average duration of the sickness which includes contagious period is approximately thirty two days (Smallpox, 2002).

The simulator is set according to the data obtained by the CDC. Figure 7 shows the parameters set for this virus. The base case has "restrict the sick" already checked to indicate that all personnel with symptoms should be restricted to their berthing. This should not be optional due to the nature of the virus. Personnel with a high fever and rash should not be working. Figure 8 shows the base graph, which displays the course of the virus with "restrict the sick" selected alongside a graph showing no precautions. Notice the rate of new infections decreases. Despite this decrease, the same number of people become infected; it just takes longer. The base graph will be used for all future comparisons specific to the smallpox virus.

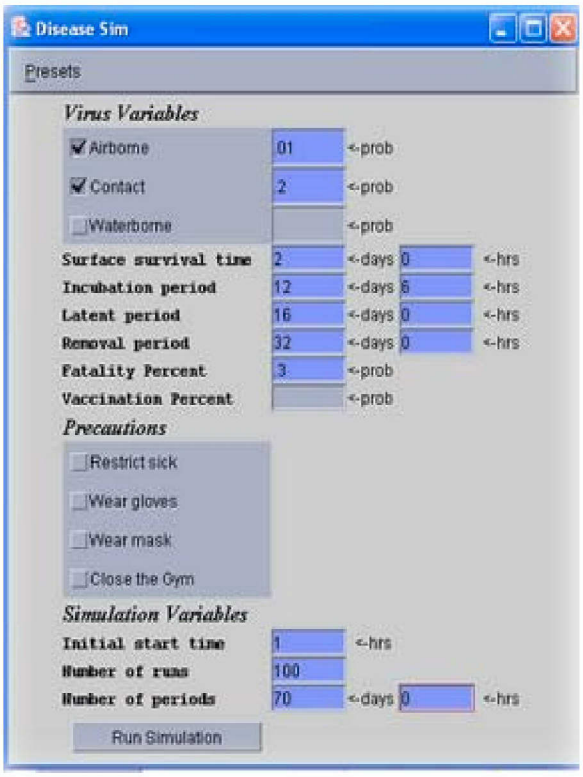

Figure 7. Smallpox parameters.

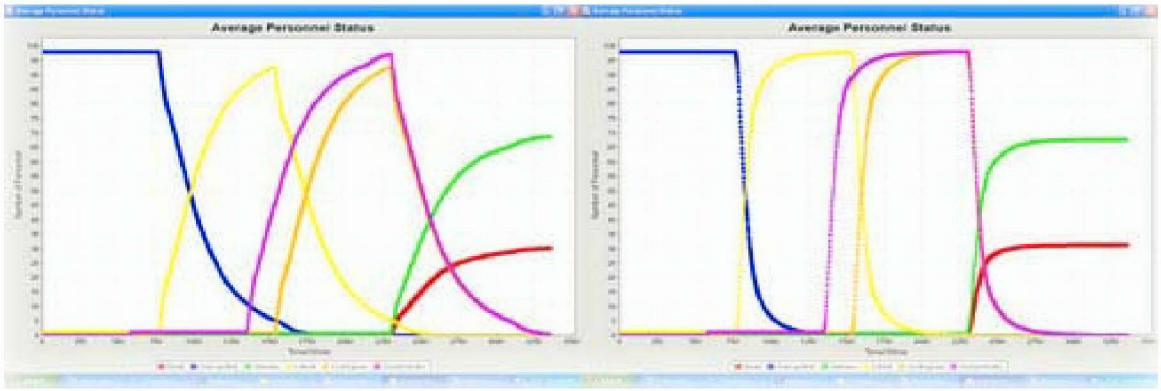

Figure 8. Comparison between restricting the sick (left) and not restricting the sick (right) during an outbreak of smallpox.

The smallpox virus was further tested with additional precautions, varied vaccination percentages, and lower contact virulence. Table 1 shows the effects of each of these changes.

Precaution	Effect to base graph
Restrict Sick	Included in base graph Shallower slopes than graph with no precautions
Restrict Sick & Wear Gloves	# infected decrease by 49% Extended disease lifetime
Restrict Sick, Wear Gloves, & Wear Mask	# infected decrease by 55% Extended disease lifetime
10% Vaccination	#infected decrease by 14%
30% Vaccination	#infected decrease by 46%
50% Vaccination	#infected decrease by 70% More people are immune or susceptible than are infected.
10% contact probability	#infected decrease by16% Extended disease lifetime
5% contact probability	#infected decrease by40% Extended disease lifetime by 21 days
1% contact probability	#infected decrease by 54% Extended disease lifetime by 50 days.

Table 1. Effects of precautionary measures on the smallpox virus.

Since the smallpox virus is primarily transmitted via contact with infected objects or personnel, wearing gloves has the greatest effect of all non-medical precautions, see Figure 9. Note: the time scale is different.

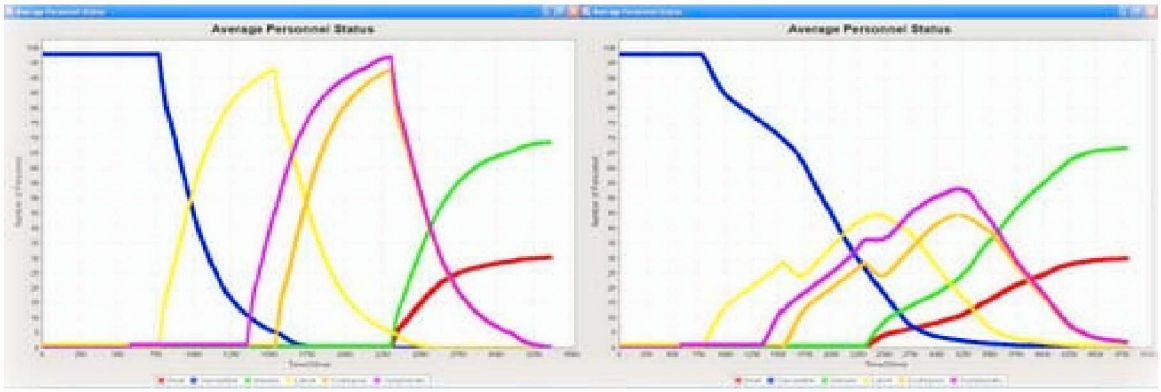

Figure 9. Comparison between the small pox base graph (left) the graph representing the effects of wearing gloves (right).

The smallpox virus has an existing vaccination that has been proven effective at preventing the disease. If a medical practitioner administers the vaccination to fifty percent of his crew with enough time for the crew members to develop immunity, the effects are drastically positive. Vaccination can even help smallpox severity after exposure if it is conducted within seven days (Whitehouse, 2002). Figure 10 shows these effects compared to the base graph. Vaccination appears to not only prevent infection for those inoculated, but it also lowers the number of new cases of infection.

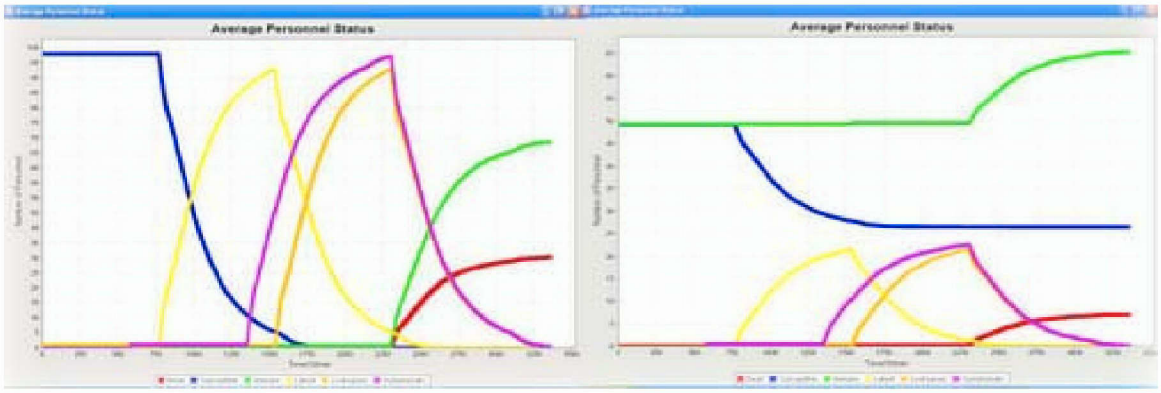

Figure 10. Comparison between the small pox base graph (left) and the graph representing the effects of vaccinating half the crew (right).

It is also speculated that the virus virulence can be reduced by additional measures. Since additional measures such as strict quarantine and improved sanitation are not modeled in the program, they can be expressed by a reduction in the probabilities of transmission. This is an example of how a simple mathematical model would account for these measures. In this case, the contact probability is reduced to one percent, to simulate improved sanitation

procedures, see Figure 11. The course of the disease is extended in time, but the total number infected remains unchanged.

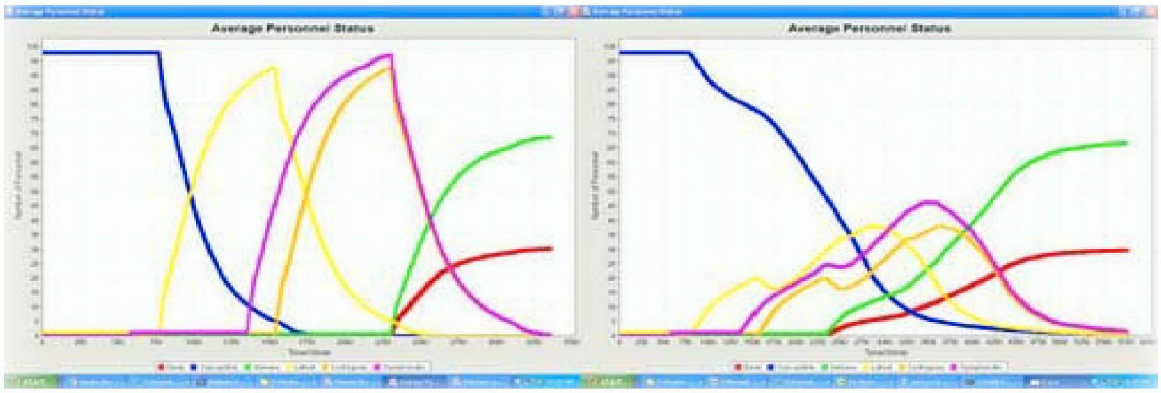

Figure 11. Comparison between the small pox base graph (left) and the graph representing a contact probability of one percent (right).

2. SARS

Severe acute respiratory syndrome (SARS) is a viral respiratory illness caused by a coronavirus. It caused a serious outbreak in 2003 that affected 8,098 people worldwide and killed 774 of them (SARS, 2004). SARS is primarily transmitted via airborne droplets from coughing or sneezing. These droplets either infect another person directly or land on a surface and infect them indirectly. Much of the specifics concerning stages of the disease are still not certain. The median incubation period is four days (Meltzer, 2004). The latent period may be shorter, but definitely starts after initial symptoms. The removal period varies significantly considering the symptoms of the disease which normally include, fever, and pneumonia. The fatality rate is approximately fifteen percent (SARS, 2003).

The airborne and contact probabilities are set to ten percent, see Figure 12. The chances of touching something

infected and being coughed or sneezed on are subjectively chosen, but should be relatively close to one another. Surface survival time is set to six hours to reflect the time a surface remains infected. The incubation period is set to the median of four days and the latent period is set to a slightly shorter period. The removal period is set to fourteen days, but is adjusted in the analysis. The fatality percent is set at fifteen. Since infected individuals have high fever, they are required to stay in their quarters.

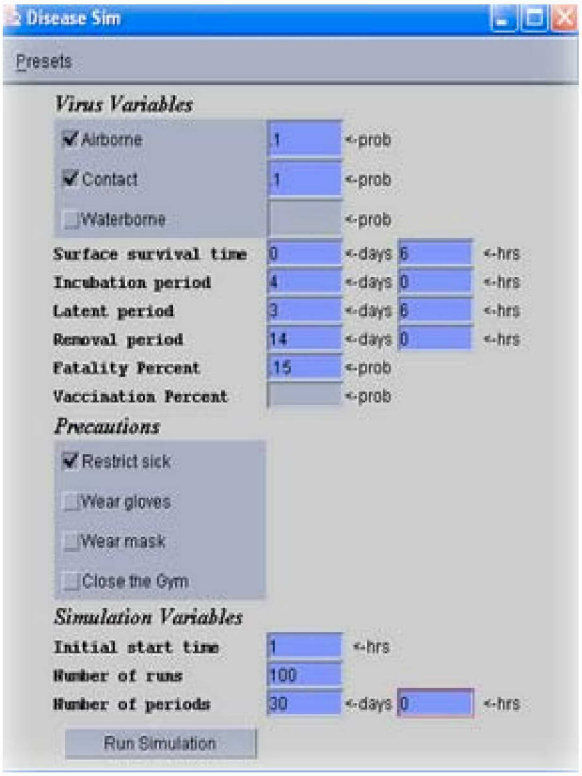

Figure 12. SARS parameters

The base settings for the SARS virus yielded the graph displayed in Figure 13. The base settings include, restrict the sick, due to the high fever and respiratory problems of the virus. The graph does not change significantly without this precaution; the cause of

infection does change however. Hatches and ladders are nearly eliminated as causes due to the bed rest and limited movement of the host.

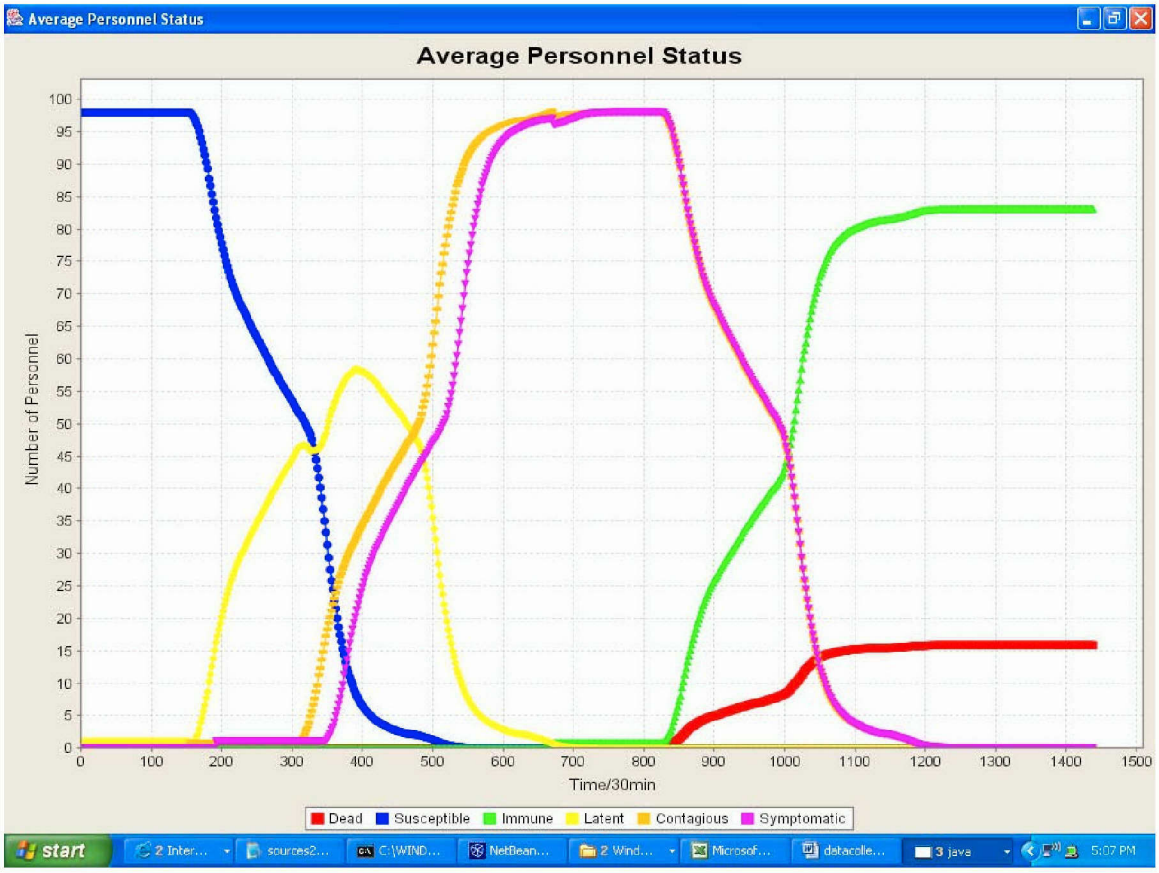

Figure 13. SARS basic graph

The effects of various precautions are displayed in Table 2. The best combination of precautions, restrict the sick, wear gloves, and wear a mask, yield the graph in Figure 14. In the graph, the maximum number of infected at the same time is reduced by fifty three percent. The total infected remains unchanged however. Although no infections are prevented, the crew is not incapacitated at the same time as in the basic graph.

Precaution	Effect to base graph
Restrict Sick	Reduces contact via hatches and ladders Slight shift to right
Wear Gloves	Reduces contact by 90% Significant shift to right Shorter contagious peak duration Extended disease lifetime
Wear Mask	Reduces airborne by 92% Minor shift to the right
Restrict Sick & Wear Gloves	Relative to Wearing gloves, there is a small shift to the right
Restrict Sick, Wear Gloves, & Wear Mask	Reduces infected by 53% Extended disease lifetime by 22 days Total infected remains unchanged

Table 2. Effects of precautionary measures on the SARS virus.

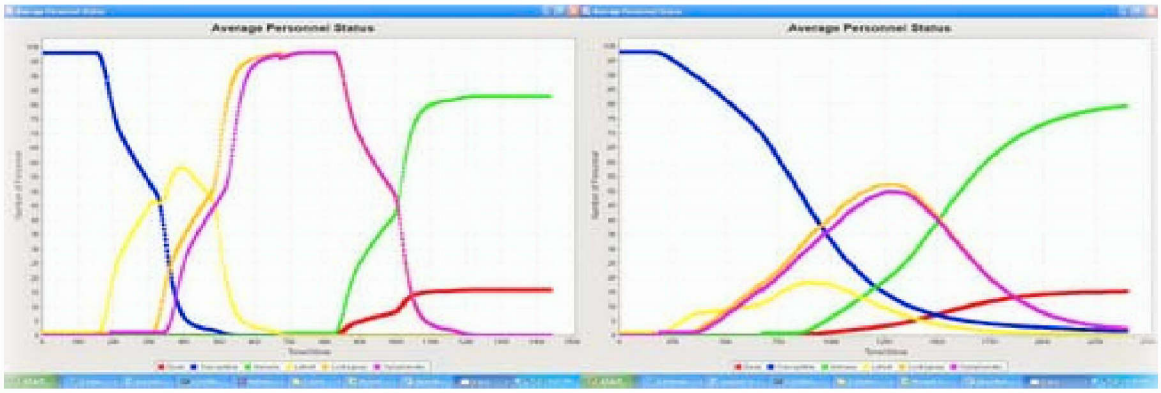

Figure 14. Comparison between the SARS base graph (left) and the graph representing the combined effects of restricting the sick, wearing gloves, and wearing a mask (right).

Since the removal period varies widely depending on the individual, it was adjusted to note how the characteristics change. Figure 15 shows the effect of lowering the removal period to ten days while Figure 16 shows the effect of raising it to twenty. It basically extends or shortens the virus lifetime starting at the peak of the contagious stage.

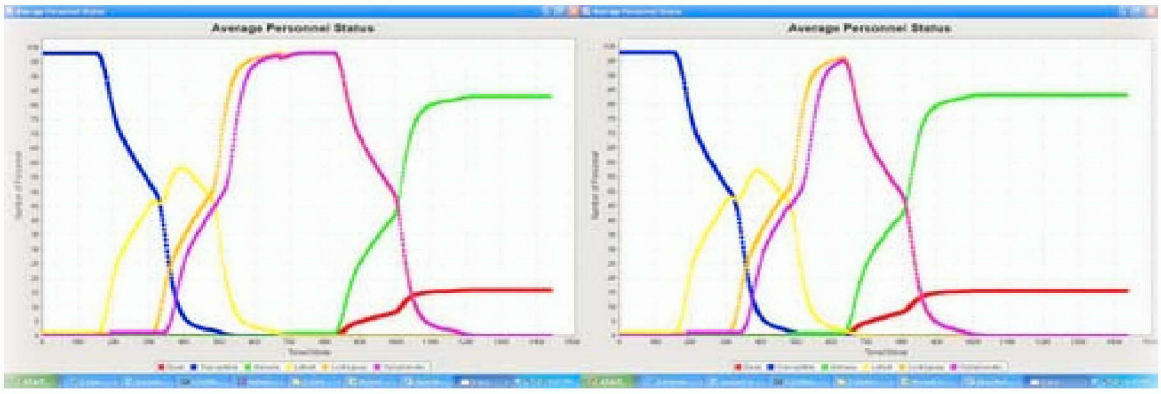

Figure 15. Comparison between the SARS base graph (left) and the graph representing the effect of lowering removal time to ten days (right).

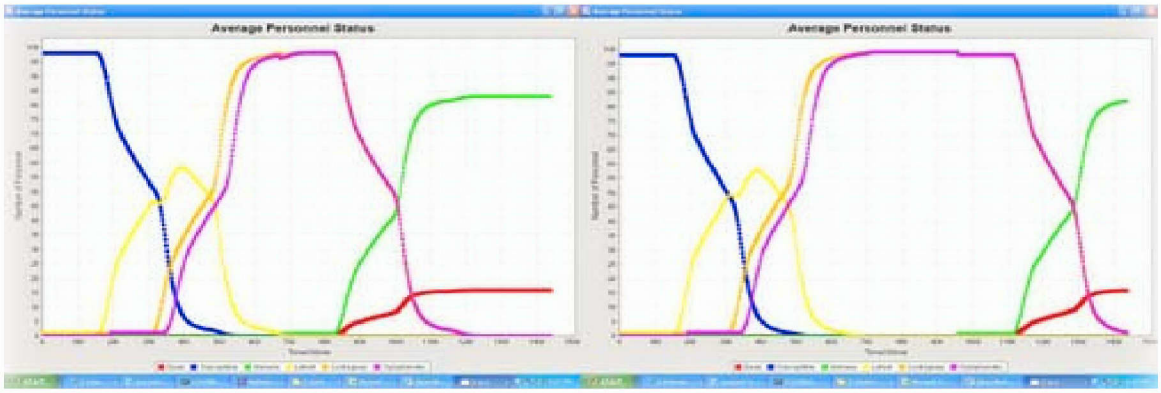

Figure 16. Comparison between the SARS base graph (left) and the effect of raising the removal time to twenty days (right).

Due to the lack of vaccination for the SARS virus, vaccination options were not explored. Since the virus is spread by both airborne and contact means, both must be countered to make an impact. The best way to deal with the SARS virus is clearly to wear masks and gloves. They have a synergistic effect on defending against the virus.

3. Norovirus

The term norovirus describes a group of viruses that cause the "stomach flu." They have similar transmission,

stages, and symptoms. Contamination is caused by vomit or fecal matter from an infected individual. A norovirus can be transmitted via contaminated food, drink, surfaces, or in close contact with an infected individual. The most prevalent form of transmission is via food and drink (Norovirus Q&A, 2005).

> Prevention of foodborne norovirus disease is based on the provision of safe food and water. Noroviruses are relatively resistant to environmental challenge: they are able to survive freezing, temperatures as high as 60°C, and have even been associated with illness after being steamed in shellfish. Moreover, noroviruses can survive in up to 10 ppm chlorine, well in excess of levels routinely present in public water systems (Norovirus Tech, 2005).

The incubation period is one to two days and the latent period closely coincides with incubation. Recovery is fairly quick, approximately one to two days from the time symptoms occur. Fatalities are not connected with these viruses; they are more annoying than dangerous. Vaccination is not a likely solution, due to the many forms of the virus. Immunity is only effective against the same strain of the virus.

The probabilities associated with the different forms of transmission (waterborne, airborne, and contact) were arbitrarily chosen according to the likelihood of infection as interpreted from Center of Disease Control (CDC) information. The base case has waterborne set at ten percent, contact at five percent, and airborne at one percent, see Figure 17. Surface survival time, is set at one hour, assuming vomit or feces is cleaned up within that period. The incubation, latent, and removal periods are set according to CDC statistics. No precautions are set,

because the disease is not serious enough to warrant mandatory precautions. The base graph is depicted in Figure 18.

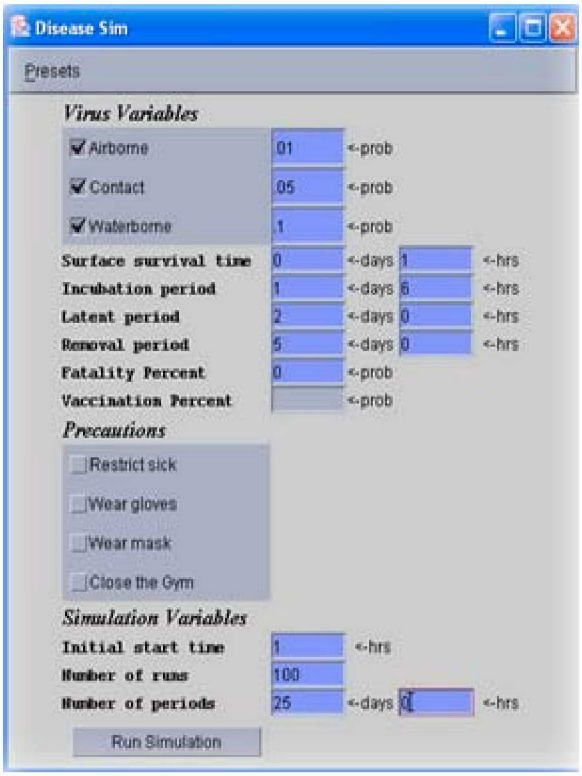

Figure 17. Norovirus parameters

Figure 18. Norovirus base graph

Of the non-medical precautions, restricting the sick and wearing gloves show slightly positive results, see Figure 19. The effects of other precautions are displayed in Table 3.

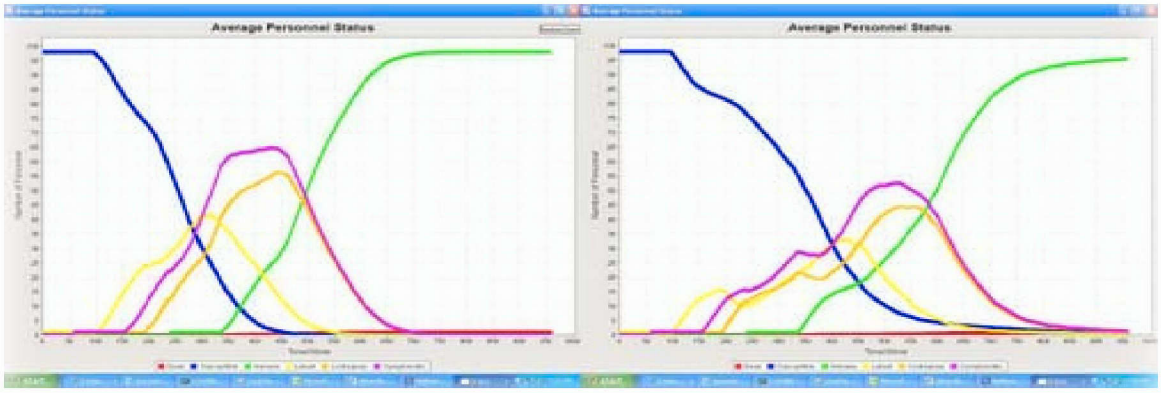

Figure 19. Comparison between the norovirus base graph (left) and the combined effects of restricting the sick and wearing gloves (right).

Precaution	Effect to base graph
Restrict Sick	# of max infected decreased by 5% Extends disease lifetime by 2 days Less duration at contagious peak
Wear Gloves	# of max infected decreased by 3% Slight shift to right
Wear Mask	No significant change
Restrict Sick & Wear Gloves	# of max infected decreased by 12% Extends disease lifetime by 5 days

Table 3. Effects of precautionary measures on the norovirus.

The proper way to combat a waterborne disease like the norovirus is through proper food handling techniques and good personal hygiene. These techniques are indirectly modeled by lowering the waterborne probability parameter. The results of lowering this parameter significantly affects the number of maximum infected at one time by twenty seven percent. The life of the virus is extended by ten days and the speed at which the virus takes hold is slowed, see Figure 20.

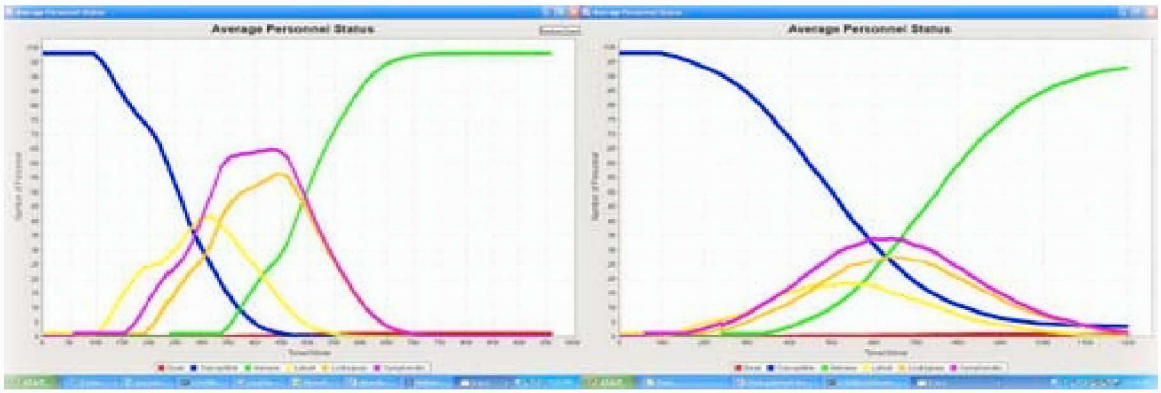

Figure 20. Comparison between the norovirus base graph (left) and the graph representing the effects of a waterborne transmission probability of one percent (right).

V. CONCLUSION

A. SUMMARY

The goal of this thesis was to create a disease simulation that was specific to Navy ships for use by medical practitioners. This goal has partially been met, but there still is much to do before the simulation is ready for real world use.

A simulation makes it possible to represent effects and interventions at a high level of detail. We can reduce a transmission coefficient in a simple math model to represent closing the gym, but would that really give the same result?

It is possible to write down a simulation as a set of equations, but this set might be too large to solve by hand. They might even be too large to give to an automated differential equation solver (i.e. a program for solving ordinary differential equations (ODE)). Even if you did, the complexity of the system would make it unlikely that one would learn anything without a graphical summary like the one presented in this thesis. And finally, you would still be missing stochastic (random) effects.

B. FUTURE WORK

There is always room for improvement with any program or model. A significant amount of enhancements are necessary before the program created in this thesis is ready for experimental use. These enhancements are listed below:

- Hull specific model – The number of compartments, their size, and arrangement along

with crew size and routines are all variables that affect the outcome of a simulation. The databases that are used for the ship and the crew must be filled with accurate data to get a more accurate approximation of disease spread.

- Enhanced routine – The current model only uses the basic elements of a person's routine. It does not cover exceptions such as multiple workspaces or unusual working hours. The simulation would be improved by using specific routines and working hours for each individual. This can be added to the database and interpreted by the program.

- Vaccination records – A record of vaccination for all personnel onboard should be kept in a separate database. Since immunization to one disease does not normally transfer to others, the doctor should be able to select the disease and have the program determine who is immunized from the relevant database.

- Variable virus stage periods - In most cases, the incubation, latent, and removal periods are variable in time. The computer simulation currently uses the mean periods, it can be improved by using probability to give different period lengths within a range of values.

- Ship visualization – In order to better understand what personnel are sick, where they are located and how they interact, a visual

display showing this type of information could be created.

- Intelligent agents – The agents used in this thesis are simple and do not learn. It may be interesting to introduce learning agents that know when other agents are exhibiting symptomatic behavior and react accordingly.
- Readiness conditions - Navy ships have various readiness conditions that change routine significantly. Alternate routines could be changed with readiness condition.

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